SCSO Page 1 of 7



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RAW SEQUENCE LISTING

FATENT APPLICATION: US/09/673,166A

- PATE: 12/26/2802 - TIME: 13:30:33

Input Set : A:\19624051.app

Output Set: N:\CRF4\12262002\1673166A.raw

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1102 AFFLICANT: 1e Gal, Frederique Anno
         Guillet, Jean Gerard
         Schery-Segard, Hanne
         Gras-Masse, Helene
         Melnyk, Oleg
         Tartar, Andre
10 <120> Title of invention: Lifofeffides inducing t lymphocytic cytotoxicity
        BEARING AT LEAST ONE AUXILIARY T EFITOFE, AND USES FOR
         VACCINATION
14 0130> FILE REFERENCE: 102.174
    140 > CURRENT APPLICATION NUMBER: 09/673,166A
16
17 < 141 > CURRENT FILING DATE: 2001+04-04
19 kises Prior Application NUMBER: PCT/Fk99/00792
20 :1815 PRIOR FILING DATE: 1999-04-06
22 <160> NUMBER OF SEQ ID NOS: 276
24 <170> SOFTWARE: Fatentin Ver. 2.1
26 K2105 BEU ID NO: 1
20 <211> LENGTH: 14
28 - 2012 * TYPE: PRT
   -213> OKGANISM: Clostridium tetanus
31 KARCH FEATURE:
   <223> OTHER INFORMATION: amino acids 830-843 of the tetanus toxin
34 <400> SEQUENCE: 1
35 Gin Tyr lle Lys Ala Ash Ser Lys Pho Ile Gly He Thr Glu
36
39 CORNERS OF MORE
40 kull - LENGTH: 14
41 K212% TYPE: FRT
40 <213 CRGANISM: Human Papillomavirus (HFV)
44 J2205 FRATURE:
48 SINS CTHER INFORMATION: uninc wride 4s=: 1 st HEV ET protein
47 8400 S SECTEMBER 1
Ar Gly Gin Ala Glu Fro Asp And Ala His Ash lie Val The Fie
English OFF IN No. 3
Provide LENGTH: Le
MARKEL STREET
to elico de anion: Artificial departo
POST PERCEPTION
PHONOLOGY NAMES WHY: COMIC
1.4 \times 1.1.1 \times 10^{12} \text{ Will W:}
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Input Not : A:\19624051.app
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Re der Dor. En Tyr lie lys Ala Asn Der lys Phe lie Gly lie Thr Blu
r. 4
66 Ala Ala Ala Ala Ala Diy Ile Gly Ile Lea Thr Val
e7
70 (160) SEQ ID NO: 4
Mi willy LEMGTH: 1>
72 Z1ZG TYFE: FRT
73 //132 ORGANISM: Artificial Requesses
75 - 2205 FEATURE:
76 - 2215 NAME/KEY: LIFT
77 1220 EQUATION: (1)
78 | L252 OTHER INFORMATION: dipaimitcyl-lysyl chain on N-terminal residue
80 /400> SEQUENCE: 4
81 Ser Ser Gln Tyr Ile Lys Ala Ash Ser Lys Phe Ile Gly Ile Thr Glu
82 1
{\it F4} Arg Gly Arg Ala Ala Gly II.e Gly Ile Leu Thr Val
   2.0
48 <210> SEQ ID NO: 5
e9 <2112 LENGTH: 28
90 - 212 TYPE: PRT
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 KEETS NAME/KEY: LIPID
95 <222 LOCATION: (1)
96 < 203 : OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue
98 <4005 SEQUENCE: 5
99 Gly Arg Gln Tyr Ile Lys Ala Ash Ser Lys Phe Ile Gly Ile Thr Gld
100 1
100 Ard Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val
       20
103
106 <210> SEQ ID NO: 6
107 k2115 LENGTH: 28
108 COIDS TYPE: PRT
109 - Vib> ORGANISM: Artificial Sequence
III KAZON PEATURE:
IID KOOD NAMEZKEY: LIFID
113 K2225 LOCATION: (1)
114 <723> OTHER INFORMATION: monopalmitoyl-lysyl chain on N-terminal residue
 16 84005 BEQUENCE: 6
117 See Ser Win Tyr lie lys Ala Ash See lys Ene lie Wly lie Thr Wo
Looking Gly Arm Ala Ala Gly The Gly The Let The Val
11.4 - 1.1 - 25, 10 No. 7

11.4 - 1.1 - 150 TH: 25

11.6 - 21. - THEE: 157

11.7 - 21. - 38, AND AND AND SELECTION
PRATTER:
THE RELEASE NAME FROM THE
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EATENT ABBLICATION: US/09/673,166A TIME: 13:30:33

RAW SEQUENCE LISTING

DATE: 1272672.02

FATENT APPLICATION: US/09/673,166A - TIME: 13:30:33 Input Net : A:\19624051.app www.gut det: N:\CRF4\12262002\I673166A.raw 131 - - 14 2577 20:: 131 km/sk CTHER INFORMATION: monoralmit velejesel shain on Newerminal regidue 134 K47AV JEGTENME: 0 lef Gly Ary Gir Tyr lie Lys Ala Ash Cer Lys The lie Gly lie Thr Glu 13€ 198 Arg Gly Arg Ala Ala Gly The Gly The Leu Thr Val 139 2.3 142 <210> SEQ ID NG: 8 143 <2015 LENGTH: 10 144 / 218/ TYPE: FRT 140 M2132 ORGANISM: Artificial Commence 147 - Papa FRATURE: 148 <223> OTHER INFORMATION: A hydrazine is bound between the N-terminal lysine 149 and isoleucine at position 2 151 <400> SEQUENCE: 8 152 Lys Ile Leu Lys Glu Fro Vai His Gly Val 153 1 156 <210> SEQ ID NO: 9 187 KR11: LENGTH: 15 15% <212> TYPE: FRT 159 (213> ORGANISM: Artificial Sequence 161 < 220> FEATURE: 162 (223) OTHER INFORMATION: aldehyde group bound to N- terminal residue 164 <220> FEATURE: 165 <221> NAME/KEY: LIPID 166 <222> LOCATION: (15) 167 KIZBO OTHER INFORMATION: palmittyl chain on C-terminal lysine residue 169 <400: SEQUENCE: 9 170 Arg Thr Fre Fre Ala Tyr Arg Fre Fre Ash Ala Ere lle Leu Lys 10 174 <210> SEQ ID NO: 10 175 <211> LENGTH: 9 176 <212> TYPE: PRT 197 ×213> ORGANISM: Homo sapions 179 ROSCS FRATURE: 180 x4235 OTHER INFORMATION: epitope from BCK-ABL fusion protein (chronic myeloid leukemia translocation) 193 k400> SEQUENCE: 10 184 Blu Asp Ala Glu Leu Ash Fri Ari Fhe 188 - Lik - OFÇ ID NO: 11 lay -1115 LENGTH: 4 196 KITIB TYPE: EKT 199 - 7135 BUANISM: Homosapiens 1 ** * /L / * FFATURE: 44 - 72 - CTHER INFORMATION: Git que in to POR-ARD invitor protein objection 1980 — mywlidd lwdRwmia transl dati'n 1980-947 - SELMENDER 11 le Der Mallea Aspilet Mallys My Lea

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RAW SEQUENCE LISTING LATE: 12/1k/2 %. PATENT APPLICATION: US/09/673,166A TIME: 13:8:3:

Input Cert: A:\19624051.app
Output Set: N:\CRF4\12262002\1673166A.raw

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्रिक्र
2/2 //11 / PEG 10 NO: 12
2013 - 2010 - CLEMPROME: 94
LC4 2022 TYPE: ERT
198 - 21:2 CROANISM: Home sapions
207 - 227 > FEATURE:
20% SILES OTHER INFORMATION: exitors from BCB-ABL fusion protein (chronic
109 myeloid leukemia translocation)
DII 84000 SEQUENCE: 12
212 Amp Glu Leu Glu Ala Val Erk Ann Ile
216 K210> SEQ ID NO: 13
217 <211> LENGTH: 9
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <220> FEATURE:
222 <223> OTHER INFORMATION: eritope from BCR-ABL fusion protein (chronic
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225 <400> SEQUENCE: 13
126 Lys Gl: Asp Ala Leu Glm Arg Fro Val
227 1
230 <210> FEQ ID NO: 14
231 K211> LENGTH: 9
232 K2125 TYPE: FRT
233 <213> ORGANISM: Homo sapiens
235 42205 FEATURE:
236 (213) OTHER INFORMATION: epitope from BCB-ARL fusion protein (chronic
2.37
     myeloid leukemia translocation)
239 {<}400° SEQUENCE: 14
240 Glu Asp Ala Leu Gln Arg Pro Val Ala
241 1
244 <210> SEQ ID NO: 15
245 <211> LENGTH: 9
246 -2125 TYPE: FRT
247 <213 > ORGANISM: Home suplems
249 K220 FEATURE:
100 -2235 OTHER INFORMATION: opitope incm BCR-ABL jusion protoin adhrenia
         myeloid leukemia translocation)
288 k400> SEQUENCE: 18
254 Gly Glo Lys Lou Arm Val Lon Gly Tyr
Life KAINS BEQUID NO: Ie
Disk Kills ENGTH: 9
.en ships TYPE: FFT
Celebrate Obsamiom: Homo sapiens
183 W. D. & REATURE:
1944 KOUNN OTHER INPORMATIONS Apitupe in EdelARIC 1936 high team otherwist
oknoka obkomén member: ok
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RAW SEQUENCE LISTING

FATENT APELICATION: US/09/673,166A TIME: 19:1:13

TIATE: IL/200/2002

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The No Asp The Met His Val Eld Flor the
2. 6. 04
LVA KAIK KOEÇ ID MO: OT
203 KOTI + LENGTE: →
074 - 2125 TYPE: FRT
176 File ORGANISM: Home satisfies
277 - 3200 PEATURE:
276 × 223× DOHER INFORMATION: epitopo from BOB-ABL tusion protein (chronic
279 myeldid leukemia translomation)
281 × 4000 SEQUENCE: 17
182 Met Gla Tyr Leu Gli Lys Lys Ash Ehe
2. 70 %
Z86 KI105 BEQ ID NO: 18
287 <211> LENGTH: 9
288 KI12  TYPE: PRT
289 <213> DRGANISM: Homo sariens
291 <220> FEATURE:
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297 1
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302 <2120 TYPE: PRT
303 <213> ORGANISM: Home sapiens
305 < 2200 FEATURE:
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307 myeloid leukemia translocation)
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310 Val Ash Gln Glu Arg Phe Arg Met Ile
311 1
314 <210> SEQ ID NO: 20
315 KMIIN LENGTH: 9
316 <211 > TYPE: PRT
317 k2135 ORGANISM: Hemo sapiens
319 K22C> FEATURE:
320 <2235 OTHER INFORMATION: epitope from BCR-ABL tusion protein (chronic
         myeloid leukemia translocation)
323 K4005 BEQUENCE: 20
374 Leu Phe Gin Lys Leu Ala Per Jin Leu
ala kalah segilah mo: di
BAR KATIS DEMOTE: +
-- PLINSTYPE: PET
aki kulak akamiam: Hara sapikaa
BEN WILLIAM HEATURE:
484 RELEASE CHEER INFORMATION: Report profit to PTE-ARL tost organization community
    myelkii leeskemia transil tatlin
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VERIFICATION SUMMARYDATE: 1.028/2017FATENT ABBLICATION: US/09/673,166ATIME: 1::51:34

Input Vet : A:\19624051.app

butput Vet: N:\CRF4\12262002\1673166A.raw